

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re: Abad, et al.  
Appl. No.: To Be Assigned  
Filed: Concurrently Herewith  
For: GENES ENCODING NOVEL PROTEINS WITH PESTICIDAL ACTIVITY  
AGAINST COLEOPTERANS

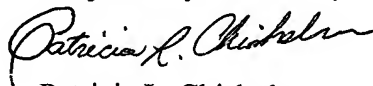
**STATEMENT IN SUPPORT OF FILING A  
SEQUENCE LISTING UNDER 37 CFR § 1.821(f)**

Box Patent Application  
Commissioner for Patents  
Washington, DC 20231

Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted concurrently herewith in accordance with 37 CFR § 1.821(c) and (e), are the same.

Respectfully submitted,



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Date of Deposit: October 23, 2001

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Pamela Lockley

**CERTIFICATE OF MAILING**

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner For Patents, Washington, DC 20231, on October 23, 2001.

# SEQUENCE LISTING

<110> Andre R. Abad  
 Nicholas B. Duck  
 Xiang Feng  
 Ronald D. Flannagan  
 Theodore W. Kahn  
 Lynn E. Sims

<120> Genes Encoding Novel Proteins With  
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 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp  
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 Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys  
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 Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn  
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 Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val  
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 Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala  
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 Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys  
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 Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp  
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 Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu  
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 Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro  
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Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly	
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Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
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Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
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Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
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ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat ctt caa	1152
Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln	
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caa atg tat gga act aat caa aat cta cac agc act agt acc ttt gat	1200
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
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ttt acg aat tat gat att tac aag act cta tca aag gat gca gta ctc	1248
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
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ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga atg cca	1296
Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro	
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Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr	
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Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp	
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Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu	
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Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly	
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Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala	
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Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala	
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Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro	
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gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt tct	1680
Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser	
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Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn		270
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Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg		285
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Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val		320
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Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr		335
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Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln		365
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Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp		380
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Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu		400
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	450	455
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu		460
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Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro		525
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Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser		540
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Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val		575
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Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr		605
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Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg		640
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Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
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cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
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tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
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agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
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cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg caa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp	
100 105 110	
gag att ttt atg gaa caa gta gaa gaa ctc ata aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
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130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg aaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Trp Lys Glu Asn Pro	
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Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg		
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Arg	Glu	Met	Thr	Leu	Thr	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Asn		
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Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg		
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Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	Tyr		
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Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala		
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Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu		
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ctt	gat	att	gtt	ttt	cct	ggg	tat	acg	tat	ata	ttt	ttt	gga	atg	cca	1296	
Leu	Asp	Ile	Val	Phe	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro		
			420					425					430				
gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	acc	aga	aag	acg	1344	
Glu	Val	Glu	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr			
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tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg ggt 1488  
 Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly  
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 Asp Leu Ile Asn Ala Val His Ser Asp Lys Ile Thr Gln Ile Pro Val  
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 Tyr Ala Thr Leu Pro Pro Ile Lys Phe Thr Thr Thr Glu Pro Phe Ile  
 625 630 635 640

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Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu
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Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr
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Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Gln	Lys	Ser	Gln	Trp
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Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala
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Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu
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Ser	Glu	Leu	Glu	Leu	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn	Tyr	Glu	
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Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	Pro	Ala	Thr	Gly
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Val	Lys	Val	Ser	Asp	Leu	Ala	Pro	Ser	Ile	Thr	Gly	Gly	Pro	Asn	Asn

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 Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala  
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 Gln Lys Thr Met Asn Arg Gly Glu Ala Leu Thr Tyr Asn Lys Phe Asn  
                     610                      615                      620  
 Tyr Ala Thr Leu Pro Pro Ile Lys Phe Thr Thr Thr Glu Pro Phe Ile  
 625                      630                      635                      640  
 Thr Leu Gly Ala Ile Phe Glu Ala Glu Asp Phe Leu Gly Ile Glu Ala  
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<221> misc\_feature  
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 <223> mo1218-1

<400> 9  
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 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
   1                    5                    10                    15  
 tcc acc tcc gtg tcc aac gac tcc aac cgc tac ccc ttc gcc aac gag 96  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
                     20                    25                    30  
 ccc acc aac gcc ctc cag aac atg gac tac aag gac tac ctc aag atg 144  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
                     35                    40                    45  
 tcc gcc ggc aac gcc tcc gag tac ccc ggc tcc ccc gag gtg ctc gtg 192  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
   50                    55                    60  
 tcc ggc cag gac gcc gcc aag gcc gcc atc gac atc gtg ggc aag ctc 240  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
   65                    70                    75                    80  
 ctc tcc ggc ctc ggc gtg ccc ttc gtg ggc ccc atc gtg tcc ctc tac 288  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
                     85                    90                    95  
 acc cag ctc atc gac atc ctc tgg ccc tcc ggc gag aag tcc cag tgg 336  
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
                     100                    105                    110

gaa atc ttc atg gag cag gtg gag gag ctc atc aac cag aag atc gcc Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala 115 120 125	384
gag tac gcc cgc aac aag gcc ctc tcc gag ctg gag ggc ctc ggc aac Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn 130 135 140	432
aac tac cag ctc tac ctc acc gcc ctg gag gag tgg gag gag aac ccc Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro 145 150 155 160	480
aac ggc tcc cgc gcc ctc cgc gac gtg cgc aac cgc ttc gag atc ctc Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu 165 170 175	528
gac tcc ctc ttc acc cag tac atg ccc tcc ttc cgc gtg acc aac ttc Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe 180 185 190	576
gag gtg ccc ttc ctc acc gtg tac gcc atg gcc gcc aac ctc cac ctc Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu 195 200 205	624
ctc ctc ctc aag gac gcc tcc atc ttc ggc gag gag tgg ggc tgg tcc Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser 210 215 220	672
acc acc acc atc aac aac tac tac gac cgc cag atg aag ctc acc gcc Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala 225 230 235 240	720
gag tac tcc gac cac tgc gtg aag tgg tat gag acc ggc ctc gcc aag Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys 245 250 255	768
ctc aag ggc acc tcc gcc aag cag tgg gtg gac tac aac cag ttc cgc Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg 260 265 270	816
cgc gag atg acc ctc gcc gtg ctc gac gtg gtg gcc ctc ttc ccc aac Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn 275 280 285	864
tac gac acc cgc acc tac ccc atg gag acc aag gcc cag ctc acc cgc Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg 290 295 300	912
gag gtg tac acc gac ccg ctc ggc gcc gtg aac gtg tcc tcc atc ggc Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly 305 310 315 320	960
tct tgg tac gac aag gcc cca agc ttc ggc gtg atc gag tcc tcc gtg Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val 325 330 335	1008
atc cgc ccg ccg cac gtg ttc gac tac atc acc ggc ctc acc gtg tac Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr 340 345 350	1056
acc cag tcc cgc tcc atc tcc tcc gcc cgc tac atc cgc cac tgg gcc Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala 355 360 365	1104



610

615

620

acc ctc aac ctc gcc acc gac tcc tcc ctc gcc ctc aag cac aac ctc 1920  
 Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu  
 625 630 635 640

ggc gag gac ccc aac tcc acc ctc tcc ggc atc gtg tac gtg gac cgc 1968  
 Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg  
 645 650 655

atc gag ttc atc ccc gtg gac gag acc tac gag gcc gag tga 2010  
 Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu \*  
 660 665

&lt;210&gt; 10

&lt;211&gt; 669

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Maize optimized Cry1218-1

&lt;400&gt; 10

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 1 5 10 15  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 50 55 60  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 65 70 75 80  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
 85 90 95  
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
 100 105 110  
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
 115 120 125  
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
 130 135 140  
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro  
 145 150 155 160  
 Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu  
 165 170 175  
 Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe  
 180 185 190  
 Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu  
 195 200 205  
 Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser  
 210 215 220  
 Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala  
 225 230 235 240  
 Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys  
 245 250 255  
 Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg  
 260 265 270  
 Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn  
 275 280 285  
 Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg  
 290 295 300

Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly  
 305 310 315 320  
 Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val  
 325 330 335  
 Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr  
 340 345 350  
 Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala  
 355 360 365  
 Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln  
 370 375 380  
 Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp  
 385 390 395 400  
 Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu  
 405 410 415  
 Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro  
 420 425 430  
 Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr  
 435 440 445  
 Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp  
 450 455 460  
 Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu  
 465 470 475 480  
 Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly  
 485 490 495  
 Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala  
 500 505 510  
 Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala  
 515 520 525  
 Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro  
 530 535 540  
 Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser  
 545 550 555 560  
 Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala  
 565 570 575  
 Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val  
 580 585 590  
 Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro  
 595 600 605  
 Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr  
 610 615 620  
 Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu  
 625 630 635 640  
 Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg  
 645 650 655  
 Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu  
 660 665

<210> 11  
 <211> 2022  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
 <221> CDS  
 <222> (1)...(2022)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> NGSR.N1218-1

<400> 11  
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Met	Ser	Pro	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Thr	Pro	
1				5					10					15		
tct	act	tct	gta	tcc	aat	gat	tct	aac	aga	tac	cct	ttt	gcg	aat	gag	96
Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu	
			20					25				30				
cca	aca	aat	gcg	cta	caa	aat	atg	gat	tat	aaa	gat	tat	tta	aaa	atg	144
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met	
		35					40				45					
tct	gcg	gga	aat	gct	agt	gaa	tac	cct	ggg	tca	cct	gaa	gta	ctt	gtt	192
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val	
	50					55				60						
agc	gga	caa	gat	gca	gct	aag	gcc	gca	att	gat	ata	gta	ggg	aaa	tta	240
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu	
	65				70				75						80	
cta	tca	ggg	tta	ggg	gtc	cca	ttt	gtt	ggg	ccg	ata	gtg	agt	ctt	tat	288
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr	
			85					90						95		
act	caa	ctt	att	gat	att	ctg	tgg	cct	tca	ggg	gaa	aag	agt	caa	tgg	336
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp	
		100						105					110			
gaa	att	ttt	atg	gaa	caa	gta	gaa	gaa	ctc	att	aat	caa	aaa	ata	gca	384
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala	
		115					120					125				
gaa	tat	gca	agg	aat	aaa	gcg	ctt	tcg	gaa	tta	gaa	gga	tta	ggg	aat	432
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn	
	130					135					140					
aat	tac	caa	tta	tat	cta	act	gcg	ctt	gaa	gaa	tgg	gaa	gaa	aat	cca	480
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro	
	145				150				155					160		
aat	ggg	tca	aga	aat	ggg	tcc	cgg	gcc	tta	cga	gat	gtg	cga	aat	cga	528
Asn	Gly	Ser	Arg	Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	
			165					170					175			
ttt	gaa	atc	ctg	gat	agt	tta	ttt	acg	caa	tat	atg	cca	tct	ttt	aga	576
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	
		180						185					190			
gtg	aca	aat	ttt	gaa	gta	cca	ttc	ctt	act	gta	tat	gca	atg	gca	gcc	624
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	
		195					200					205				
aac	ctt	cat	tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	gaa	672
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	
	210						215				220					
tgg	gga	tgg	tca	aca	act	act	att	aat	aac	tat	tat	gat	cgt	caa	atg	720
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	
	225				230					235				240		
aaa	ctt	act	gca	gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	act	768
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	
			245					250						255		

ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	







Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys  
595 600 605  
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala  
610 615 620  
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu  
625 630 635 640  
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val  
645 650 655  
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala  
660 665 670  
Glu

<210> 13  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>

<223> NGS Insert

<400> 13  
aatggttccc gg

12

<210> 14  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>

<223> NGS Insert

<400> 14  
Asn Gly Ser Arg  
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<210> 15  
<211> 2010  
<212> DNA  
<213> Bacillus thuringiensis (truncated)

<220>

<221> CDS

<222> (1)...(2010)

<221> misc\_feature

<222> (0)...(0)

<223> 1218-1A

<400> 15

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Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96  
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144  
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met





gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt tct	1680
Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser	
545 550 555 560	
gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa gca	1728
Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala	
565 570 575	
ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att gta	1776
Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val	
580 585 590	
ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac cca	1824
Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro	
595 600 605	
ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc aca	1872
Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr	
610 615 620	
aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat tta	1920
Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu	
625 630 635 640	
ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac cga	1968
Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg	
645 650 655	
atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa taa	2010
Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *	
660 665	

<210> 16  
 <211> 669  
 <212> PRT  
 <213> Bacillus thuringiensis (truncated)

<400> 16

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Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu	
165 170 175	
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe	



<210> 17  
 <211> 2022  
 <212> DNA  
 <213> Bacillus thuringiensis (truncated)

<220>  
 <221> CDS  
 <222> (1)...(2022)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> 1218-2A

<400> 17  
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 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
 85 90 95

act caa ctt att gat att ctg tgg cct tca ggg caa aag agt caa tgg 336  
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp  
 100 105 110

gag att ttt atg gaa caa gta gaa gaa ctc ata aat caa aaa ata gca 384  
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
 115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432  
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
 130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg aaa gaa aat cca 480  
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro  
 145 150 155 160

aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg 528  
 Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu  
 165 170 175

gat agt tta ttt acg caa tac atg cca tct ttt cga gtg aca aat ttt 576  
 Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe  
 180 185 190

gaa gta cca ttc ctt aca gta tat aca cag gca gcc aac ctt cat tta 624







<212> PRT

<213> Bacillus thuringiensis (truncated)

<400> 18

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
1 5 10 15  
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
20 25 30  
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
35 40 45  
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
50 55 60  
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
65 70 75 80  
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
85 90 95  
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp  
100 105 110  
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
115 120 125  
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
130 135 140  
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro  
145 150 155 160  
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu  
165 170 175  
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe  
180 185 190  
Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu  
195 200 205  
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser  
210 215 220  
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala  
225 230 235 240  
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys  
245 250 255  
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg  
260 265 270  
Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn  
275 280 285  
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg  
290 295 300  
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly  
305 310 315 320  
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val  
325 330 335  
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr  
340 345 350  
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala  
355 360 365  
Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys  
370 375 380  
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp  
385 390 395 400  
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu  
405 410 415  
Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro  
420 425 430  
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr  
435 440 445  
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Gly Thr Arg Asp  
450 455 460  
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu



aaa ata gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga	291
Lys Ile Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly	
80 85 90	
tta ggt aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa	339
Leu Gly Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu	
95 100 105 110	
gaa aat cca aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt	387
Glu Asn Pro Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe	
115 120 125	
gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg	435
Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val	
130 135 140	
aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac	483
Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn	
145 150 155	
ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg	531
Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp	
160 165 170	
gga tgg tca aca act act att aat aac tat tat gat cgt caa atg aaa	579
Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys	
175 180 185 190	
ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt	627
Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly	
195 200 205	
tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac	675
Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn	
210 215 220	
caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta	723
Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu	
225 230 235	
ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa	771
Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln	
240 245 250	
cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct	819
Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser	
255 260 265 270	
tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa	867
Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu	
275 280 285	
tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc	915
Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu	
290 295 300	
aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata aga	963
Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg	
305 310 315	
cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt	1011
His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser	
320 325 330	



575                      580                      585                      590

cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac    1827  
 His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr  
                     595                      600                      605

ggt gac cga atc gaa ttc atc cca gta gat taa                      1860  
 Val Asp Arg Ile Glu Phe Ile Pro Val Asp \*  
                     610                      615

<210> 20  
 <211> 616  
 <212> PRT  
 <213> Bacillus thuringiensis (truncated)

<400> 20  
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   1                    5                    10                    15  
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys  
                     20                    25                    30  
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu  
                     35                    40                    45  
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
                     50                    55                    60  
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
                     65                    70                    75                    80  
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
                     85                    90                    95  
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn  
                     100                    105                    110  
 Pro Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile  
                     115                    120                    125  
 Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn  
                     130                    135                    140  
 Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His  
                     145                    150                    155                    160  
 Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp  
                     165                    170                    175  
 Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr  
                     180                    185                    190  
 Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala  
                     195                    200                    205  
 Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe  
                     210                    215                    220  
 Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro  
                     225                    230                    235                    240  
 Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr  
                     245                    250                    255  
 Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile  
                     260                    265                    270  
 Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser  
                     275                    280                    285  
 Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val  
                     290                    295                    300  
 Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp  
                     305                    310                    315                    320  
 Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu  
                     325                    330                    335  
 Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe  
                     340                    345                    350  
 Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val  
                     355                    360                    365

10032717-1003304

Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met  
 370 375 380  
 Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys  
 385 390 395 400  
 Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg  
 405 410 415  
 Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr  
 420 425 430  
 Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr  
 435 440 445  
 Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser  
 450 455 460  
 Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro  
 465 470 475 480  
 Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly  
 485 490 495  
 Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly  
 500 505 510  
 Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys  
 515 520 525  
 Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile  
 530 535 540  
 Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn  
 545 550 555 560  
 Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile  
 565 570 575  
 Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn  
 580 585 590  
 Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp  
 595 600 605  
 Arg Ile Glu Phe Ile Pro Val Asp  
 610 615

<210> 21  
 <211> 2022  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
 <221> CDS  
 <222> (1)...(2022)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> LKMS.N1218-1

<400> 21  
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 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15  
 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30  
 cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45  
 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Glu Val Leu Val  
 50 55 60



agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
tta aaa atg tct aat ggt tca aga gcc tta cga gat gtg cga aat cga	528
Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	



Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala  
565 570 575

tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat 1776  
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp  
580 585 590

gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa 1824  
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys  
595 600 605

aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca 1872  
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala  
610 615 620

gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg 1920  
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu  
625 630 635 640

aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt 1968  
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val  
645 650 655

tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg 2016  
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala  
660 665 670

gaa taa  
Glu \* 2022

<210> 22  
<211> 673  
<212> PRT  
<213> Bacillus thuringiensis (mutated)

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1 5 10 15  
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
20 25 30  
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
35 40 45  
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
50 55 60  
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
65 70 75 80  
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
85 90 95  
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
100 105 110  
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
115 120 125  
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
130 135 140  
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro  
145 150 155 160  
Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg  
165 170 175  
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg  
180 185 190  
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala

195	200	205
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu		
210	215	220
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met		
225	230	235
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr		240
245	250	255
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr		
260	265	270
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala		
275	280	285
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala		
290	295	300
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val		
305	310	315
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile		320
325	330	335
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly		
340	345	350
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile		
355	360	365
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly		
370	375	380
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr		
385	390	395
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys		400
405	410	415
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe		
420	425	430
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn		
435	440	445
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala		
450	455	460
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln		
465	470	475
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile		480
485	490	495
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr		
500	505	510
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr		
515	520	525
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val		
530	535	540
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg		
545	550	555
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala		560
565	570	575
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp		
580	585	590
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys		
595	600	605
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala		
610	615	620
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu		
625	630	635
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val		640
645	650	655
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala		
660	665	670
Glu		

<210> 23  
 <211> 2013  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
 <221> CDS  
 <222> (1)...(2013)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> LKMS.R1218-1

<400> 23  
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48  
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
 85 90 95

act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336  
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
 100 105 110

gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384  
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
 115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432  
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
 130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480  
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro  
 145 150 155 160

tta aaa atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa atc 528  
 Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile  
 165 170 175

ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat 576  
 Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn  
 180 185 190

ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat 624

Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His	
195 200 205	
tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga tgg	672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp	
210 215 220	
tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt act	720
Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr	
225 230 235 240	
gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca	768
Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala	
245 250 255	
aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa ttc	816
Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe	
260 265 270	
cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc cca	864
Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro	
275 280 285	
aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca	912
Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr	
290 295 300	
agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att	960
Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile	
305 310 315 320	
ggg tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc	1008
Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser	
325 330 335	
gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg	1056
Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val	
340 345 350	
tat aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg	1104
Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp	
355 360 365	
gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat ctt	1152
Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu	
370 375 380	
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gtaaatgttt atttaaaaga gaacgcatga gtagacacct tctttcattt ataaaatatc 6600  
actgatggaa ttc 6613

<210> 29  
<211> 1863  
<212> DNA  
<213> Bacillus thuringiensis (mutated)

<220>  
<221> CDS  
<222> (1)...(1863)  
<221> misc\_feature  
<222> (0)...(0)  
<223> NGS.R49PVD

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ggt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa 96  
Val Ser Gly Gln Asp Ala Ala Lys Ala Ile Asp Ile Val Gly Lys  
20 25 30  
tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144  
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu  
35 40 45  
tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192  
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
50 55 60  
tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240  
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
65 70 75 80  
gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288  
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
85 90 95  
aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat 336  
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn  
100 105 110  
cca aat ggt tca aga aat ggt tcc cgg gcc tta cga gat gtg cga aat 384  
Pro Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn  
115 120 125  
cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt 432

Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe	
130 135 140	
aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca	480
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala	
145 150 155 160	
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa	528
Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu	
165 170 175	
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa	576
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln	
180 185 190	
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa	624
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu	
195 200 205	
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac	672
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp	
210 215 220	
tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt	720
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val	
225 230 235 240	
gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa	768
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	
245 250 255	
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac	816
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	
260 265 270	
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg	864
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	
275 280 285	
ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg	912
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr	
290 295 300	
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat	960
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr	
305 310 315 320	
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg	1008
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg	
325 330 335	
ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc	1056
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser	
340 345 350	
act agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca	1104
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser	
355 360 365	
aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata	1152
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile	
370 375 380	

ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat	1200
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn	
385 390 395 400	
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata	1248
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile	
405 410 415	
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat	1296
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp	
420 425 430	
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt	1344
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser	
435 440 445	
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg	1392
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp	
450 455 460	
aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc	1440
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile	
465 470 475 480	
act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca	1488
Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro	
485 490 495	
gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat	1536
Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn	
500 505 510	
aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta	1584
Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu	
515 520 525	
gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act	1632
Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr	
530 535 540	
gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca	1680
Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro	
545 550 555 560	
aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt	1728
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val	
565 570 575	
gca gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca	1776
Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala	
580 585 590	
ttg aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata	1824
Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile	
595 600 605	
gtt tac gtt gac cga atc gaa ttc atc cca gta gat taa	1863
Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp *	
610 615 620	

<210> 30  
<211> 620

<212> PRT

<213> *Bacillus thuringiensis* (mutated)

<400> 30

Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu  
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20 25 30  
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu  
35 40 45  
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
50 55 60  
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
65 70 75 80  
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
85 90 95  
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn  
100 105 110  
Pro Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn  
115 120 125  
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe  
130 135 140  
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala  
145 150 155 160  
Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu  
165 170 175  
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln  
180 185 190  
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu  
195 200 205  
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp  
210 215 220  
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val  
225 230 235 240  
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys  
245 250 255  
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn  
260 265 270  
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val  
275 280 285  
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr  
290 295 300  
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr  
305 310 315 320  
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg  
325 330 335  
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser  
340 345 350  
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser  
355 360 365  
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile  
370 375 380  
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn  
385 390 395 400  
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile  
405 410 415  
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp  
420 425 430  
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser  
435 440 445  
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp  
450 455 460  
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile







aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata	1152
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile	
370 375 380	
ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat	1200
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn	
385 390 395 400	
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata	1248
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile	
405 410 415	
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat	1296
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp	
420 425 430	
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt	1344
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser	
435 440 445	
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg	1392
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp	
450 455 460	
aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc	1440
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile	
465 470 475 480	
act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca	1488
Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro	
485 490 495	
gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat	1536
Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn	
500 505 510	
aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta	1584
Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu	
515 520 525	
gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act	1632
Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr	
530 535 540	
gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca	1680
Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro	
545 550 555 560	
aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt	1728
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val	
565 570 575	
gca gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca	1776
Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala	
580 585 590	
ttg aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata	1824
Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile	
595 600 605	
gtt tac gtt gac cga atc gaa ttc atc cca gta gat taa	1863
Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp *	

<210> 32  
 <211> 620  
 <212> PRT  
 <213> *Bacillus thuringiensis* (mutated)

<400> 32

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		20					25				30				
Leu	Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu
	35					40				45					
Tyr	Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln
	50				55					60					
Trp	Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile
65				70				75						80	
Ala	Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly
			85					90					95		
Asn	Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn
	100						105					110			
Pro	Leu	Lys	Met	Ser	Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn
	115					120						125			
Arg	Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe
	130				135					140					
Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala
145				150				155						160	
Ala	Asn	Leu	His	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	
			165					170					175		
Glu	Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln
	180							185					190		
Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu
	195						200					205			
Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp
	210				215						220				
Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val
225				230						235				240	
Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys
			245					250					255		
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn
		260						265					270		
Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val
	275						280					285			
Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr
	290				295					300					
Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr
	305				310					315				320	
Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg
		325						330					335		
Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser
		340						345					350		
Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser
	355						360					365			
Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile
	370				375						380				
Phe	Phe	Gly	Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn
385				390						395				400	
Asn	Thr	Arg	Lys	Thr	Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile
		405						410					415		
Ala	Ser	Thr	Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp
		420						425					430		

Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser  
 435 440 445  
 Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp  
 450 455 460  
 Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile  
 465 470 475 480  
 Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro  
 485 490 495  
 Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn  
 500 505 510  
 Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu  
 515 520 525  
 Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr  
 530 535 540  
 Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro  
 545 550 555 560  
 Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val  
 565 570 575  
 Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala  
 580 585 590  
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 595 600 605  
 Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp  
 610 615 620

<210> 33  
 <211> 1854  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
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 <221> misc\_feature  
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 gtt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa 96  
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys  
 20 25 30  
 tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144  
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu  
 35 40 45  
 tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192  
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
 50 55 60  
 tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240  
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
 65 70 75 80  
 gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288  
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
 85 90 95





Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val  
 595 600 605

gac cga atc gaa ttc atc cca gta gat taa  
 Asp Arg Ile Glu Phe Ile Pro Val Asp \*  
 610 615

1854

<210> 34  
 <211> 617  
 <212> PRT  
 <213> Bacillus thuringiensis (mutated)

<400> 34  
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 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys  
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 35 40 45  
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
 50 55 60  
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
 65 70 75 80  
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
 85 90 95  
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn  
 100 105 110  
 Pro Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu  
 115 120 125  
 Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr  
 130 135 140  
 Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu  
 145 150 155 160  
 His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly  
 165 170 175  
 Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu  
 180 185 190  
 Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu  
 195 200 205  
 Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln  
 210 215 220  
 Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe  
 225 230 235 240  
 Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu  
 245 250 255  
 Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser  
 260 265 270  
 Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser  
 275 280 285  
 Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr  
 290 295 300  
 Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His  
 305 310 315 320  
 Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn  
 325 330 335  
 Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr  
 340 345 350  
 Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala  
 355 360 365  
 Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly  
 370 375 380  
 Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg



385                      390                      395                      400  
 Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr  
                                  405                      410                      415  
 Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn  
                                  420                      425                      430  
 Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala  
                                  435                      440                      445  
 Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg  
                                  450                      455                      460  
 Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile  
 465                                   470                      475                      480  
 Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys  
                                  485                      490                      495  
 Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr  
                                  500                      505                      510  
 Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu  
                                  515                      520                      525  
 Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp  
 530                                   535                      540  
 Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met  
 545                                   550                      555                      560  
 Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala  
                                  565                      570                      575  
 Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His  
                                  580                      585                      590  
 Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val  
                                  595                      600                      605  
 Asp Arg Ile Glu Phe Ile Pro Val Asp  
 610                                   615

<210> 35  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 5' forward primer

<400> 35  
 atgagtccaa ataatacaaaa tg

22

<210> 36  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 5' reverse primer

<400> 36  
 ccgcttctaa atcttgttcc

20

<210> 37  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 3' forward primer

<400> 37  
 ggaacaagat ttagagg

17

<210> 38  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 3' reverse primer

<400> 38  
 ctcacgtct acaatcaatt catc 24

<210> 39  
 <211> 2022  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
 <221> CDS  
 <222> (1)...(2022)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> LRNS.N1218-1

<400> 39  
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48  
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
 85 90 95

act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336  
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
 100 105 110

gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384  
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
 115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432  
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Gly Leu Gly Asn  
 130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480





tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg 2016  
 Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala  
 660 665 670

gaa taa 2022  
 Glu \*

<210> 40  
 <211> 673  
 <212> PRT  
 <213> Bacillus thuringiensis (mutated)

<400> 40

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 50 55 60  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 65 70 75 80  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
 85 90 95  
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
 100 105 110  
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
 115 120 125  
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
 130 135 140  
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro  
 145 150 155 160  
 Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg  
 165 170 175  
 Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg  
 180 185 190  
 Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala  
 195 200 205  
 Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu  
 210 215 220  
 Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met  
 225 230 235 240  
 Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr  
 245 250 255  
 Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr  
 260 265 270  
 Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala  
 275 280 285  
 Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala  
 290 295 300  
 Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val  
 305 310 315 320  
 Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile  
 325 330 335  
 Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly  
 340 345 350  
 Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile  
 355 360 365  
 Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly



tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu	144
35 40 45	
tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln	192
50 55 60	
tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile	240
65 70 75 80	
gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly	288
85 90 95	
aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn	336
100 105 110	
cca tta aga atg tct aat ggt tcc cgg gcc tta cga gat gtg cga aat Pro Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn	384
115 120 125	
cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe	432
130 135 140	
aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala	480
145 150 155 160	
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu	528
165 170 175	
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln	576
180 185 190	
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu	624
195 200 205	
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp	672
210 215 220	
tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val	720
225 230 235 240	
gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	768
245 250 255	
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	816
260 265 270	
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	864
275 280 285	





530

535

540

gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca 1680  
 Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro  
 545 550 555 560

aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt 1728  
 Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val  
 565 570 575

gca gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca 1776  
 Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala  
 580 585 590

ttg aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata 1824  
 Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile  
 595 600 605

gtt tac gtt gac cga atc gaa ttc atc cca gta gat taa 1863  
 Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp \*  
 610 615 620

&lt;210&gt; 42

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Bacillus thuringiensis (mutated)

&lt;400&gt; 42

Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu  
 1 5 10 15  
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys  
 20 25 30  
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu  
 35 40 45  
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
 50 55 60  
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
 65 70 75 80  
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
 85 90 95  
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn  
 100 105 110  
 Pro Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn  
 115 120 125  
 Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe  
 130 135 140  
 Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala  
 145 150 155 160  
 Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu  
 165 170 175  
 Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln  
 180 185 190  
 Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu  
 195 200 205  
 Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp  
 210 215 220  
 Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val  
 225 230 235 240  
 Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys  
 245 250 255  
 Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn  
 260 265 270



tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
tta aga atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa atc	528
Leu Arg Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile	
165 170 175	
ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat	576
Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn	
180 185 190	
ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat	624
Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His	
195 200 205	
tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga tgg	672
Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp	
210 215 220	
tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt act	720
Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr	
225 230 235 240	
gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca	768
Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala	
245 250 255	
aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa ttc	816
Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe	



Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro  
515 520 525

gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa gga 1632  
Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly  
530 535 540

cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt 1680  
Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly  
545 550 555 560

tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa 1728  
Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys  
565 570 575

gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att 1776  
Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile  
580 585 590

gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac 1824  
Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn  
595 600 605

cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc 1872  
Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile  
610 615 620

aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat 1920  
Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn  
625 630 635 640

tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac 1968  
Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp  
645 650 655

cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa taa 2013  
Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu \*  
660 665 670

<210> 44  
<211> 670  
<212> PRT  
<213> Bacillus thuringiensis (mutated)

<400> 44  
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
1 5 10 15  
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
20 25 30  
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
35 40 45  
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
50 55 60  
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
65 70 75 80  
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
85 90 95  
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
100 105 110  
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
115 120 125

Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
 130 135 140  
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro  
 145 150 155 160  
 Leu Arg Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile  
 165 170 175  
 Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn  
 180 185 190  
 Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His  
 195 200 205  
 Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp  
 210 215 220  
 Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr  
 225 230 235 240  
 Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala  
 245 250 255  
 Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe  
 260 265 270  
 Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro  
 275 280 285  
 Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr  
 290 295 300  
 Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile  
 305 310 315 320  
 Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser  
 325 330 335  
 Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val  
 340 345 350  
 Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp  
 355 360 365  
 Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu  
 370 375 380  
 Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe  
 385 390 395 400  
 Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val  
 405 410 415  
 Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met  
 420 425 430  
 Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys  
 435 440 445  
 Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg  
 450 455 460  
 Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr  
 465 470 475 480  
 Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr  
 485 490 495  
 Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser  
 500 505 510  
 Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro  
 515 520 525  
 Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly  
 530 535 540  
 Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly  
 545 550 555 560  
 Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys  
 565 570 575  
 Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile  
 580 585 590  
 Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn  
 595 600 605  
 Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile  
 610 615 620  
 Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn

625                      630                      635                      640  
 Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp  
                          645                      650                      655  
 Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu  
                          660                      665                      670

<210> 45  
 <211> 1854  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
 <221> CDS  
 <222> (1)...(1854)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> LRMS.R49PVD

<400> 45  
 atg tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt 48  
 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu  
   1                          5                          10                          15  
 gtt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa 96  
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys  
                           20                          25                          30  
 tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144  
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu  
                           35                          40                          45  
 tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192  
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
   50                          55                          60  
 tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240  
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
   65                          70                          75                          80  
 gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288  
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
                           85                          90                          95  
 aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat 336  
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn  
                           100                          105                          110  
 cca tta aga atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa 384  
 Pro Leu Arg Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu  
                           115                          120                          125  
 atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca 432  
 Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr  
   130                          135                          140  
 aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt 480  
 Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu  
   145                          150                          155                          160  
 cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga 528  
 His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly

165	170	175	
tgg tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt			576
Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu			
180	185	190	
act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta			624
Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu			
195	200	205	
gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa			672
Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln			
210	215	220	
ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc			720
Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe			
225	230	235	240
cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta			768
Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu			
245	250	255	
aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca			816
Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser			
260	265	270	
att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca			864
Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser			
275	280	285	
tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca			912
Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr			
290	295	300	
gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata aga cat			960
Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His			
305	310	315	320
tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat			1008
Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn			
325	330	335	
ctt caa caa atg tat gga act aat caa aat cta cac agc act agt acc			1056
Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr			
340	345	350	
ttt gat ttt acg aat tat gat att tac aag act cta tca aag gat gca			1104
Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala			
355	360	365	
gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga			1152
Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly			
370	375	380	
atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga			1200
Met Pro Glu Val Glu Phe Met Val Asn Gln Leu Asn Asn Thr Arg			
385	390	395	400
aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca			1248
Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr			
405	410	415	
aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat			1296



Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn	
420 425 430	
tat gag tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg	1344
Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala	
435 440 445	
acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat cga	1392
Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg	
450 455 460	
agt gca gat tta aac aat aca ata tat tca gat aaa atc act caa att	1440
Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile	
465 470 475 480	
ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa	1488
Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys	
485 490 495	
gga cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act	1536
Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr	
500 505 510	
ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa	1584
Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu	
515 520 525	
aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat	1632
Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp	
530 535 540	
att gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg	1680
Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met	
545 550 555 560	
aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct	1728
Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala	
565 570 575	
atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat	1776
Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His	
580 585 590	
aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt	1824
Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val	
595 600 605	
gac cga atc gaa ttc atc cca gta gat taa	1854
Asp Arg Ile Glu Phe Ile Pro Val Asp *	
610 615	

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 <213> Bacillus thuringiensis (mutated)

<400> 46  
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 1 5 10 15  
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys  
 20 25 30  
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu

[illegible]

Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	Thr	Met
545					550					555					560
Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala	Asp	Ala
				565					570						575
Ile	Thr	Thr	Leu	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Leu	Ala	Leu	Lys	His
			580					585						590	
Asn	Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val	Tyr	Val
		595					600					605			
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	610					615									

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<223> LRMS Insert

<400> 47  
 ttaagaatgt ct

12

<210> 48  
 <211> 4  
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 <213> Artificial Sequence

<220>

<223> LRMS Insert

<400> 48  
 Leu Arg Met Ser  
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